

SCORE Search Results Details for Application 10573229 and Search Result 20100803_081513_us-10-573-229a-1.rni.

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This page gives you Search Results detail for the Application 10573229 and Search Result 20100803_081513_us-10-573-229a-1.rni.

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OM nucleic - nucleic search, using sw model

Run on: August 3, 2010, 10:48:53 ; Search time 1010 Seconds
(without alignments)
7445.638 Million cell updates/sec

Title: US-10-573-229A-1
Perfect score: 920
Sequence: 1 tctgtagaggggaatggctg.....acccccaaagaaaccttcta 920

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13418083 seqs, 4087008042 residues

Total number of hits satisfying chosen parameters: 26836166

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /ABSS/Data/CRF/ptodata/2/ina/1_COMB.seq:*
- 2: /ABSS/Data/CRF/ptodata/2/ina/5_COMB.seq:*
- 3: /ABSS/Data/CRF/ptodata/2/ina/6A_COMB.seq:*
- 4: /ABSS/Data/CRF/ptodata/2/ina/6B_COMB.seq:*
- 5: /ABSS/Data/CRF/ptodata/2/ina/7A_COMB.seq:*
- 6: /ABSS/Data/CRF/ptodata/2/ina/7B_COMB.seq:*
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- 11: /ABSS/Data/CRF/ptodata/2/ina/HB_COMB.seq:*
- 12: /ABSS/Data/CRF/ptodata/2/ina/PCTUS_COMB.seq:*
- 13: /ABSS/Data/CRF/ptodata/2/ina/PP_COMB.seq:*
- 14: /ABSS/Data/CRF/ptodata/2/ina/RE_COMB.seq:*
- 15: /ABSS/Data/CRF/ptodata/2/ina/backfiles1.seq:*

SUMMARIES

Result	% Query						Description
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	1	322.2	35.0	650	10	US-09-925-065A-602935	Sequence 602935,
	2	309.8	33.7	501	10	US-09-925-065A-602938	Sequence 602938,
	3	149.6	16.3	485	10	US-09-925-065A-425353	Sequence 425353,
	4	122.6	13.3	561	3	US-09-573-080A-108	Sequence 108, App
	5	122.6	13.3	561	5	US-09-854-867-108	Sequence 108, App
	6	121.2	13.2	541	3	US-09-573-080A-107	Sequence 107, App
	7	121.2	13.2	541	5	US-09-854-867-107	Sequence 107, App
c	8	119.6	13.0	493	10	US-09-925-065A-176178	Sequence 176178,
c	9	119.6	13.0	504	11	US-10-301-480C-643499	Sequence 643499,
c	10	109.6	11.9	590	10	US-09-925-065A-73587	Sequence 73587, A
c	11	109.6	11.9	590	10	US-09-925-065A-73588	Sequence 73588, A
c	12	109.6	11.9	590	11	US-10-301-480C-550895	Sequence 550895,
c	13	109.6	11.9	590	11	US-10-301-480C-550896	Sequence 550896,
	14	104.8	11.4	737	7	US-10-105-299-6677	Sequence 6677, Ap
	15	104.8	11.4	797	7	US-10-105-299-234	Sequence 234, App
c	16	104.8	11.4	137000	3	US-10-172-911-11	Sequence 11, Appl
c	17	98.4	10.7	84105	6	US-10-741-601-5637	Sequence 5637, Ap
c	18	98	10.7	55927	3	US-09-949-016-15017	Sequence 15017, A
c	19	97.8	10.6	9245	3	US-09-949-016-13349	Sequence 13349, A
c	20	97.8	10.6	9245	3	US-09-949-016-13350	Sequence 13350, A
	21	93	10.1	948	11	US-10-301-480C-92013	Sequence 92013, A
c	22	91.8	10.0	143550	3	US-09-949-016-14143	Sequence 14143, A
	23	91.2	9.9	992	11	US-10-301-480C-220057	Sequence 220057,
	24	90.8	9.9	76118	3	US-09-949-016-15593	Sequence 15593, A
	25	90.4	9.8	806	11	US-10-301-480C-325534	Sequence 325534,
	26	90.2	9.8	564	10	US-09-925-065A-236350	Sequence 236350,
	27	90.2	9.8	574	11	US-10-301-480C-695058	Sequence 695058,
	28	89.4	9.7	589	11	US-10-301-480C-427272	Sequence 427272,
	29	89.4	9.7	589	11	US-10-301-480C-427274	Sequence 427274,
	30	89.4	9.7	589	11	US-10-301-480C-605967	Sequence 605967,
	31	89.4	9.7	592	10	US-09-925-065A-134131	Sequence 134131,
	32	89	9.7	589	11	US-10-301-480C-427273	Sequence 427273,
	33	88.4	9.6	987	11	US-10-301-480C-932619	Sequence 932619,
c	34	86.6	9.4	660	11	US-10-301-480C-296865	Sequence 296865,
c	35	85.4	9.3	870	11	US-10-301-480C-296866	Sequence 296866,
	36	85.2	9.3	463	10	US-09-925-065A-594086	Sequence 594086,
	37	85.2	9.3	575	10	US-09-925-065A-333372	Sequence 333372,
	38	85.2	9.3	577	11	US-10-301-480C-783034	Sequence 783034,
	39	85.2	9.3	986	11	US-10-301-480C-163837	Sequence 163837,
	40	85.2	9.3	987	11	US-10-301-480C-950354	Sequence 950354,
	41	85.2	9.3	987	11	US-10-301-480C-950355	Sequence 950355,
	42	84.8	9.2	915	8	US-10-098-754-678	Sequence 678, App
	43	84.2	9.2	997	11	US-10-301-480C-326425	Sequence 326425,
	44	84.2	9.2	55927	3	US-09-949-016-15017	Sequence 15017, A
c	45	84	9.1	601	3	US-09-949-016-178228	Sequence 178228,

ALIGNMENTS

RESULT 1
US-09-925-065A-602935

; Sequence 602935, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 602935
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-602935

Query Match 35.0%; Score 322.2; DB 10; Length 650;
Best Local Similarity 95.4%;
Matches 354; Conservative 0; Mismatches 13; Indels 4; Gaps 2;

Qy	373	GCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTACGTGGAGTGAAAAC	432
Db	1	GCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTACGTGGAGTGAAAAC	60
Qy	433	TTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAATTTCTCTGCTTC	492
Db	61	TTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAATTTCTCTGCTTC	120
Qy	493	TGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCTCCCTG	552
Db	121	TGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCTCCCTG	180
Qy	553	CCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAAATCGAGAGACCTCTA	612
Db	181	CCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAAATCGAGAGACCTCTA	240
Qy	613	ACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGA	672
Db	241	ACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGA	300
Qy	673	AGTACCTGCTGGGTTCTGGGGGTTGGGGAAGGAAAATCCCTACTGCCCCAAGAGCCAGCC	732
Db	301	AGTACCTGCTGG---TTCTGGGGTTGGGGAGGAAGATCCCTACTG-CCCAAGAGCCAGCA	356
Qy	733	CCGAACCCAAG	743

Db 357 CAGACACAAGG 367

RESULT 2

US-09-925-065A-602938
; Sequence 602938, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 602938
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-602938

Query Match 33.7%; Score 309.8; DB 10; Length 501;
Best Local Similarity 94.5%;
Matches 343; Conservative 0; Mismatches 17; Indels 3; Gaps 2;

Qy	381	ACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTACGTGGAGTGAAAACCTTTAAGGG	440
Db	1	ACTGAGAAGCATCACCCACTTCCCCAGAGCCTTTTTTACATGGAGTGAAAACCTTTAAGGG	60
Qy	441	GCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAATTTCTCTGCTTCTGCAAAAAG	500
Db	61	GCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAAGTTCTCTGCTTCTGCAAAAAG	120
Qy	501	GACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCCTCCCTGCCCCAGGC	560
Db	121	GACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCCTCCCTGCCCCAGGC	180
Qy	561	CCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATCGAGAGACCTCTAACCTGGG	620
Db	181	CCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATCGAAAGACCTCTAACCTGGG	240
Qy	621	AGAGGAGGGAGGGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGAAGTACCTG	680
Db	241	AGAGGAGGGAGGGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGAAGTACCTG	300
Qy	681	CTGGGTTCTGGGGGTTGGGGAAGGAAAATCCCTACTGCCCAAGAGCCAGCCCCGAACCC	740

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          |||| | |||| ||| |||| |||||||| ||||||||| ||| |
Db      301 CTGG--TTCTGGGGTCAGGGGAGGAAGATCCCTACTG-CCCAAGAGCCAGCACAGACACA 357

Qy      741 AAG 743
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Db      358 AGG 360
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RESULT 3

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US-09-925-065A-425353
; Sequence 425353, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 425353
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-425353
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Query Match          16.3%; Score 149.6; DB 10; Length 485;
Best Local Similarity 91.0%;
Matches 193; Conservative 0; Mismatches 14; Indels 5; Gaps 3;
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Qy      532 ACGGGGGTAAAACCTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAA 591
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Db      1 ACGGGGGTAAAACCTTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAA 60

Qy      592 GGTAGAATCGAGAGACCTCTAACCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGG 651
          ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Db      61 GGTAGAATCGAGAGACCTCTAA-CCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGG 119

Qy      652 GTTATGCAACAACACAAGGGAAGTACCTGCTGGGTTCTGGGGTTGGGGAAGGAAAATCC 711
          ||||||||| ||||||||| ||||||||| ||| | ||| ||||| ||||
Db      120 GTTATGCAACAACACAAGGGAAGTACCTGCTG---TTCTGGGGTTGGGAGGAAGATCC 176

Qy      712 CTACTGCCCCAAGAGCCAGCCCCGAACCCAAG 743
          ||||| ||||||||| ||| | | |
Db      177 CTACTG-CCCAAGAGCCAGCACAGACACAAGG 207
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Db 381 TGA CTGCAGCCCCAGCTAACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACC 440

Qy 228 CCCTGGCTAAATTGCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276

Db 441 ACCCAGCTAAGCTGCTCCTAAATTCCTGACCCACAGAAACTGTGAGAGA 489

RESULT 5

US-09-854-867-108

; Sequence 108, Application US/09854867

; Patent No. 7014997

; GENERAL INFORMATION:

; APPLICANT: JOAN, KNOLL H

; APPLICANT: ROGAN, PETER K

; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME

; FILE REFERENCE: 30307

; CURRENT APPLICATION NUMBER: US/09/854,867

; CURRENT FILING DATE: 2003-05-08

; NUMBER OF SEQ ID NOS: 613

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 108

; LENGTH: 561

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: repeat_region

; LOCATION: (1)..(561)

; OTHER INFORMATION: mlt1f1

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (62)..(62)

; OTHER INFORMATION: n is a, c, g or t

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (165)..(165)

; OTHER INFORMATION: n is a, c, g or t

US-09-854-867-108

Query Match 13.3%; Score 122.6; DB 5; Length 561;

Best Local Similarity 69.6%;

Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;

Qy 2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGAGAGGTGC 61

Db 201 CTCTGGGGGAAGCCAGCTGCCATGTCATGAGGACACTCAAGCAGCCCTGTGGAGAGGCC 260

Qy 62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACCACTGCACTAACCTGCTGGGTC----- 114

Db 261 ATGTGGCAAGGAAGTGAAGCCTCCTGCCAACAGCCAGCAAGGAAGTGAAGCCTCCTGCCA 320

Qy 115 -----TGAGACTGAGCCACTTTGGAAGCTGATCTTGAGACACCAGTCAAGCCCTTAGC 167

Db 321 ACAGCCATGTGAGTGAGCCATCTTGGAAGCAGATCCTCCAGCCCCAGTCAAGCCTTCAGA 380

Qy 168 TGGCTGCAGCCACAGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATC 227

US-09-573-080A-107

Query Match 13.2%; Score 121.2; DB 3; Length 541;
Best Local Similarity 68.8%;
Matches 190; Conservative 3; Mismatches 81; Indels 2; Gaps 2;

http://es/ScoreAccessWeb/GetItem.action?AppId=1057322...03_081513_us-10-573-229a-1.mi&ItemType=4&startByte=0 (8 of 17)8/28/2010 8:52:28 PM


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Qy      121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
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Db      316 TGAGCCATCTTGGAAGCGGATCCTCCAGCCCCAGTYAAGCCTTCAGATGACTGCAGCCCC 375

Qy      181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
        || ||| | ||||| |||| || | || ||||| || || |||| |
Db      376 GGCTGACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACTACCCAGCTAAGCT 435

Qy      241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
        ||||| :|||| | ||||| |||| ||| | |
Db      436 GCTCCTARATTCTTGACCCACAGAACTGTGAGATA 471
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RESULT 7

US-09-854-867-107

; Sequence 107, Application US/09854867

; Patent No. 7014997

; GENERAL INFORMATION:

; APPLICANT: JOAN, KNOLL H

; APPLICANT: ROGAN, PETER K

; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME

; FILE REFERENCE: 30307

; CURRENT APPLICATION NUMBER: US/09/854,867

; CURRENT FILING DATE: 2003-05-08

; NUMBER OF SEQ ID NOS: 613

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 107

; LENGTH: 541

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: repeat_region

; LOCATION: (1)..(541)

; OTHER INFORMATION: mlt1f

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (179)..(179)

; OTHER INFORMATION: n is a, c, g or t

US-09-854-867-107

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Query Match      13.2%; Score 121.2; DB 5; Length 541;
Best Local Similarity 68.8%;
Matches 190; Conservative 3; Mismatches 81; Indels 2; Gaps 2;
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Qy      2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
        || | || || |||| || ||| | | ||||| | ||||| || |
Db      197 CTCTGGGGGAAGCCAGCTGCCATGCTATGAAGACACTCAAGCAGCCTA-TGGAGAAGTCC 255

Qy      62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACACCTGCACTAACCTGCTGGGTCTGAGAC 120
        || ||| || ||| || | || ||||| || || ||||:||| | || ||
Db      256 ACGTGGAAGGAAGTCTCCTGCCAACAGCCAGCTTCGACYTGCCAGCCATGTGAG 315

Qy      121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
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Db      316 TGAGCCATCTTGGAAGCGGATCCTCCAGCCCCAGTYAAGCCTTCAGATGACTGCAGCCCC 375
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Qy      181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
      || ||| | ||||| ||| | || ||||| ||| ||| |
Db      376 GGCTGACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACTACCCAGCTAAGCT 435

Qy      241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
      ||||| :||| | ||||| ||| | |
Db      436 GCTCCTARATTCTTGACCCACAGAACTGTGAGATA 471
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RESULT 8

US-09-925-065A-176178/c

; Sequence 176178, Application US/09925065A

; Patent No. H002191

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 176178

; LENGTH: 493

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-176178

Query Match 13.0%; Score 119.6; DB 10; Length 493;
Best Local Similarity 66.7%;
Matches 184; Conservative 1; Mismatches 90; Indels 1; Gaps 1;

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Qy      2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
      || | ||| ||||| ||||| ||| | | ||||| || ||||| |
Db      419 CTCTGGAGGAAGTCAGCTGCTGTGTCATGAGGGCACTCAAACAGCCCTATGAAGAGGTCC 360

Qy      62 ACTTGGTGAGAAACCGATGCC-TCTGCCAACACCTGCACTAACCTGCTGGGTCTGAGAC 120
      | ||| || ||| || | | ||||| || ||| |||| ||| ||| |||
Db      359 ATGTGGTAAGGAAGTGAAGTCTGCTGCAACAGCCAGCAATAACTTGCCAGGTATGTGAA 300

Qy      121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
      || ||| ||||| | | | | ||| |||| || | ||| ||| |
Db      299 TGTGCCATCTTGGAAGCAAGTTCTCCAACCTCCAGACAAGCTCTCTAATAACTGTGGCCCC 240

Qy      181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
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Db      239 AGCTGACATCTTGGCTGCAACCCACGAGGGAATCTGAGCCAGCACCACCAAGMTAAGCC 180
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Qy 241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
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RESULT 9

US-10-301-480C-643499/c
; Sequence 643499, Application US/10301480C
; Patent No. H002220
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-137
; CURRENT APPLICATION NUMBER: US/10/301,480C
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 643499
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480C-643499

Query Match 13.0%; Score 119.6; DB 11; Length 504;
Best Local Similarity 66.7%;
Matches 184; Conservative 1; Mismatches 90; Indels 1; Gaps 1;

Qy 2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
| | | | | | | | | | | | | | | | | |
Db 430 CTCTGGAGGAAGTCAGCTGCTGTGTCATGAGGGCACTCAAACAGCCCTATGAAGAGGTCC 371

Qy 62 ACTTGGTGAGAAACCGATGCC-TCTGCCAACACCTGCACTAACCTGCTGGGTCTGAGAC 120
| | | | | | | | | | | | | | | | | |
Db 370 ATGTGGTAAGGAAGTCTGAGGACTTCTGCCAACAGCCAGCAATAACTTGCCAGGTATGTGAA 311

Qy 121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
| | | | | | | | | | | | | | | | | |
Db 310 TGTGCCATCTTGGAAGCAAGTTCTCCAACCTCCAGACAAGCTCTCTAATAACTGTGGCCCC 251

Qy 181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
| | | | | | | | | | | | | | | | | |
Db 250 AGCTGACATCTTGGCTGCAACCCACGAGGGAATCTGAGCCAGCACCACCAAGMTAAGCC 191

Qy 241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
| | | | | | | | | | | | | | | | | |
Db 190 ACTCCTAAATTCCTGACTTGCAGAAAATGTGTGAAA 155

RESULT 10

US-09-925-065A-73587/c
; Sequence 73587, Application US/09925065A

; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73587
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-73587

Query Match 11.9%; Score 109.6; DB 10; Length 590;
Best Local Similarity 63.8%;
Matches 166; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 17 GCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACC 76
||| | ||||| || | ||| | | ||| | | |||
Db 299 GCTTCCATGTCATGAGGATATTCCAGCAATTCTATTAAGAGTCCACATGGCAAGGAACTG 240

Qy 77 GATGCCTCTGCCAACCACTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAG 136
| ||||| ||| || ||| | | || | ||| | |||||
Db 239 AGGTCTTCTGCCAACCAACCAGCATTAACATTCCAGGCTTGTGGGTGAGTCCCTTTGGAAG 180

Qy 137 CTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACT 196
| ||| | || ||||| || || || |||| | ||| | | ||
Db 179 CAGATCCTCCAGACTCAGTCAAGCCATCAGATGACTGCAGTCCCAGGTGATGCCCAAGCT 120

Qy 197 GCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAA 256
||||| | ||||| ||||| | | |||| | ||| | ||| |
Db 119 GCAACCTCAAGAAAGATCCTGAGCCAGAACCACTCAGCTAAGTAGCTCTCAGGTTCTGA 60

Qy 257 CCCACAGAAATTGTGTAAGA 276
|| ||| || ||||| ||
Db 59 CCTACAGCAACTGTGTGAGA 40

RESULT 11
US-09-925-065A-73588/c
; Sequence 73588, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73588
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-73588

Query Match 11.9%; Score 109.6; DB 10; Length 590;
Best Local Similarity 63.8%;
Matches 166; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 17 GCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACC 76
||| | ||||| || | ||| | | ||| | | |||
Db 299 GCTTCCATGTCATGAGGATATTCCAGCAATTCTATTAAGAGTCCACATGGCAAGGAAGT 240

Qy 77 GATGCCTCTGCCAACCACTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAG 136
| ||||| || || ||| | | || | ||| | |||||
Db 239 AGGTCTTCTGCCAACCAACAGCATTAACTCCAGGCTTGTGGGTGAGTCCCTTTGGAAG 180

Qy 137 CTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACT 196
| |||| | || ||||| || || || ||||| | ||| | | |||
Db 179 CAGATCCTCCAGACTCAGTCAAGCCATCAGATGACTGCAGTCCCAGGTGATGCCCAAGCT 120

Qy 197 GCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAA 256
|||||| | ||||| ||||| | | |||| | ||| | ||| | |
Db 119 GCAACCTCAAGAAAGATCCTGAGCCAGAACCACTCAGCTAAGTAGCTCTCAGGTTCTGA 60

Qy 257 CCCACAGAAATTGTGTGAAGA 276
|| |||| || |||| |||
Db 59 CCTACAGCAACTGTGTGAGA 40

RESULT 12
US-10-301-480C-550895/c
; Sequence 550895, Application US/10301480C
; Patent No. H002220
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-137

; CURRENT APPLICATION NUMBER: US/10/301,480C
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 550895
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480C-550895

Query Match 11.9%; Score 109.6; DB 11; Length 590;
Best Local Similarity 63.8%;
Matches 166; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 17 GCTGCTGTGTCATGGGGGTGCATGAGCAGCCAGTGGAGAGGTGCACTTGGTGAGAAACC 76
||| | ||||| || | ||| | | ||| | | |||
Db 299 GCTTCATGTCATGAGGATATTCCAGCAATTCTATTAAGAGTCCACATGGCAAGGAAGT 240

Qy 77 GATGCCTCTGCCAACACCTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAG 136
| ||||| ||| || ||| | | || | ||| | |||||
Db 239 AGGTCTTCTGCCACAACCAGCATTAAACATTCCAGGCTTGTGGGTGAGTCCCTTTGGAAG 180

Qy 137 CTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACT 196
| ||| | || ||||| || || || |||| | ||| | | ||
Db 179 CAGATCCTCCAGACTCAGTCAAGCCATCAGATGACTGCAGTCCCAGGTGATGCCCAAGCT 120

Qy 197 GCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAA 256
|||||| | ||||||||| || | |||| | ||| | ||| |
Db 119 GCAACCTCAAGAAAGATCCTGAGCCAGAACCACTCAGCTAAGTAGCTCTCAGGTTCTGA 60

Qy 257 CCCACAGAAATTGTGTAAGA 276
|| ||| || |||| |||
Db 59 CCTACAGCAACTGTGTGAGA 40

RESULT 13
US-10-301-480C-550896/c
; Sequence 550896, Application US/10301480C
; Patent No. H002220
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-137
; CURRENT APPLICATION NUMBER: US/10/301,480C
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 550896

; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480C-550896

Query Match 11.9%; Score 109.6; DB 11; Length 590;
Best Local Similarity 63.8%;
Matches 166; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy	17	GCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACC	76
Db	299	GCTTCCATGTCATGAGGATATTCCAGCAATTCTATTAAGAGTCCACATGGCAAGGAACTG	240
Qy	77	GATGCCTCTGCCAACCACTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAG	136
Db	239	AGGTCTTCTGCCAACCAACCAGCATTAAACATTCCAGGCTTGTGGGTGAGTCCCTTTGGAAG	180
Qy	137	CTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACT	196
Db	179	CAGATCCTCCAGACTCAGTCAAGCCATCAGATGACTGCAGTCCCAGGTGATGCCCAAGCT	120
Qy	197	GCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAA	256
Db	119	GCAACCTCAAGAAAGATCCTGAGCCAGAACCCTCAGCTAAGTAGCTCTCAGGTTCTCTGA	60
Qy	257	CCCACAGAAATTGTGTGAAGA	276
Db	59	CCTACAGCAACTGTGTGAGA	40

RESULT 14
US-10-105-299-6677
; Sequence 6677, Application US/10105299
; Patent No. 7368527
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6677
; LENGTH: 737
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-6677

Query Match 11.4%; Score 104.8; DB 7; Length 737;
Best Local Similarity 68.5%;
Matches 174; Conservative 0; Mismatches 77; Indels 3; Gaps 2;

Qy	24	TGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACCGATGCCT	83
Db	398	TTTCATGAGGATACTCAAGCATTCTATGGAGAGATCCACATGGTGAGAACTGAAGCCT	457

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Qy      84 -CTGCCAACCACTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAGCTGATC 142
      || ||||  || |||| ||| ||| | | || || ||||| || |||| | |
Db      458 CCTACCAAGAGCCAGCACCAACTTGCCAGCTATGTGAATGAGCCATCTTAGAAGTGGGT 517

Qy      143 TTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACTGCAACC 202
      | ||| | |||| ||| | | || ||||| || | | ||| ||||
Db      518 CTCTAGCCCTAGTCAGGCCTTCATATGACTGCAGCCAGGGCTGATATTTTGACTACAACC 577

Qy      203 TCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAACCCACA 262
      || || | || ||||| || || |||| ||||| |||| ||| |||
Db      578 TCATGAGAGA--CTGAGCCACAACAACCTAGCTAAGAAGCTCCTGAATTCCTACCAACA 635

Qy      263 GAAATTGTGTAAGA 276
      |||| | ||| |||
Db      636 GAAACTATGTGAGA 649
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RESULT 15

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US-10-105-299-234
; Sequence 234, Application US/10105299
; Patent No. 7368527
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 234
; LENGTH: 797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-234
```

```
Query Match      11.4%; Score 104.8; DB 7; Length 797;
Best Local Similarity 68.5%;
Matches 174; Conservative 0; Mismatches 77; Indels 3; Gaps 2;
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```
Qy      24 TGTCATGGGGGTGCATGAGCAGCCAGTGGAGAGGTGCACTTGGTGAGAAACCGATGCCT 83
      | |||| || | | ||| || ||||| | ||| ||||| || ||||
Db      383 TTTCATGAGGATACTCAAGCATTCCCTATGGAGAGATCCACATGGTGAGAACTGAAGCCT 442

Qy      84 -CTGCCAACCACTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAGCTGATC 142
      || ||||  || |||| ||| ||| | | || || ||||| || |||| | |
Db      443 CCTACCAAGAGCCAGCACCAACTTGCCAGCTATGTGAATGAGCCATCTTAGAAGTGGGT 502

Qy      143 TTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACTGCAACC 202
      | ||| | |||| ||| | | || ||||| || | | ||| ||||
Db      503 CTCTAGCCCTAGTCAGGCCTTCATATGACTGCAGCCAGGGCTGATATTTTGACTACAACC 562

Qy      203 TCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAACCCACA 262
      || || | || ||||| || || |||| ||||| |||| ||| |||
Db      563 TCATGAGAGA--CTGAGCCACAACAACCTAGCTAAGAAGCTCCTGAATTCCTACCAACA 620

Qy      263 GAAATTGTGTAAGA 276
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Db | | | | | | | |
621 GAAACTATGTGAGA 634

Search completed: August 3, 2010, 11:08:25
Job time : 1172 secs

SCORE 4.0